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RAW SEQUENCE LISTING

DATE: 12/12/2002

PATENT APPLICATION: US/10/010,160

TIME: 10:50:52

Input Set : A:\SEQLIST DAVI110.001AUS.TXT

Output Set: N:\CRF4\12122002\J010160.raw

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4 <110> APPLICANT: Rosey, Everett L.
5      Strugnell, Richard A.
6      Good, Robert T,
7      King, Kendall W.
9 <120> TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
10     TREATING INFECTION BY LAWSONIA SPP.
13 <130> FILE REFERENCE: DAVI110.001AUS
15 <140> CURRENT APPLICATION NUMBER: US 10/010,160
16 <141> CURRENT FILING DATE: 2001-11-09
18 <150> PRIOR APPLICATION NUMBER: AU PR1381
19 <151> PRIOR FILING DATE: 2000-11-10
21 <150> PRIOR APPLICATION NUMBER: US 60/249,596
22 <151> PRIOR FILING DATE: 2000-11-17
24 <160> NUMBER OF SEQ ID NOS: 68
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 622
30 <212> TYPE: DNA
31 <213> ORGANISM: Lawsonia intracellularis
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)...(621)
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39 Met Ser Asp Asp Pro Ser Lys Thr Glu Lys Ala Thr Pro Lys Arg Arg
40 1          5          10          15
42 cag gaa gct cgt tct gaa ggg agt gtc cct aaa tca gaa gag gtt act   96
43 Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr
44          20          25          30
46 aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca   144
47 Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
48          35          40          45
50 ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca   192
51 Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
52          50          55          60
54 gaa tca ttt cgg ttt gag gtt aca gca cag tca gta tat gct tta ttt   240
55 Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
56 65          70          75          80
58 att tat gtt gct caa gag ata gct att tta ttg atg cca ata tta ctt   288
59 Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
60          85          90          95
62 ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca   336
63 Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala

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64          100          105          110
66 tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata 384
67 Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
68          115          120          125
70 ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga 432
71 Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
72          130          135          140
74 ctt tta cgt agt tta gtt caa gta att gtt ata ggt att gtt cca tat 480
75 Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr
76 145          150          155          160
78 atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca 528
79 Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
80          165          170          175
82 agt cct tca ggt gtg gca gat tat atg ctt aat aca gga ata gta ctt 576
83 Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
84          180          185          190
86 gtt tta tat acg cta att cct atg aca att att gca gtc gca gat 621
87 Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp
88          195          200          205
90 c 622
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93 <211> LENGTH: 207
94 <212> TYPE: PRT
95 <213> ORGANISM: Lawsonia intracellularis
97 <400> SEQUENCE: 2
98 Met Ser Asp Asp Pro Ser Lys Thr Glu Lys Ala Thr Pro Lys Arg Arg
99 1          5          10          15
100 Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr
101          20          25          30
102 Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
103          35          40          45
104 Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
105          50          55          60
106 Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
107 65          70          75          80
108 Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
109          85          90          95
110 Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala
111          100          105          110
112 Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
113          115          120          125
114 Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
115          130          135          140
116 Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr
117 145          150          155          160
118 Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
119          165          170          175
120 Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
121          180          185          190

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122 Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp
123      195                      200                      205
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 789
128 <212> TYPE: DNA
129 <213> ORGANISM: Lawsonia intracellularis
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (1)...(786)
135 <400> SEQUENCE: 3
136 atg aat tta ttt aat ttt gat cct agt atg ttt ctt agt ttt tta ctt 48
137 Met Asn Leu Phe Asn Phe Asp Pro Ser Met Phe Leu Ser Phe Leu Leu
138 1      5      10      15
140 aca ttt tta cgt att agt gtt gtc tta ttt atg ctt cct ttt ttt tct 96
141 Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser
142      20      25      30
144 att gat ggt ttt cct aat atg tta aaa gca tca ata gct ctt att cta 144
145 Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
146      35      40      45
148 act ata gtt ctt tgg ggg cgt ctt tct ctt tca gga aca caa atg cca 192
149 Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
150      50      55      60
152 gcg cat cct ttc gat cta gta ttg tta atc ata agc gag gtt ttt ctt 240
153 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
154 65      70      75      80
156 ggt att gta ttg ggg ctt gcg gta aac ttt ttc ttt gca gga att caa 288
157 Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
158      85      90      95
160 gct ggg gga gaa att ctt gct aca caa atg ggg ttt aca atg att acg 336
161 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
162      100     105     110
164 ctt gca gac cca tta act ggt aac acc aca ggt ttt att gca cat ttt 384
165 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
166      115     120     125
168 ctt tat atg gtt gct aca tta gtt ttt ctt gct ctt aat ggc cat ttg 432
169 Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
170      130     135     140
172 ttt ctt ata aaa gct ttt aca tat act ttt aaa atg gtt cca gca gga 480
173 Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
174 145     150     155     160
176 gga ctt gtt gta aga gaa att tta ttg agt gaa ctt ctt aat atg gca 528
177 Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
178      165     170     175
180 ggg atg att ttt gtt ttt gcc tta cat gtt gcg gca cca gtt atg tca 576
181 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
182      180     185     190
184 gct ctt ttt tta gta gag atc tct tta gga ctt atg gca aga gct gct 624
185 Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
186      195     200     205

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188 cct cag att cat att atg gaa gtt gga ttt cct gta aaa att ggt gta 672
189 Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
190      210      215      220
192 gga ttt ttt ttc att gga cta tta ttt act atc tta tca aaa gaa acc 720
193 Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
194 225      230      235      240
196 tat cga ttt att gca ggc cta gag gga cta ttt ttt aac tta ctt act 768
197 Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
198      245      250      255
200 gta atg ggt agt gga aaa tag 789
201 Val Met Gly Ser Gly Lys
202      260
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 262
207 <212> TYPE: PRT
208 <213> ORGANISM: Lawsonia intracellularis
210 <400> SEQUENCE: 4
211 Met Asn Leu Phe Asn Phe Asp Pro Ser Met Phe Leu Ser Phe Leu Leu
212 1      5      10      15
213 Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser
214      20      25      30
215 Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
216      35      40      45
217 Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
218      50      55      60
219 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
220 65      70      75      80
221 Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Ala Gly Ile Gln
222      85      90      95
223 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
224      100     105     110
225 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
226      115     120     125
227 Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
228      130     135     140
229 Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
230 145     150     155     160
231 Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
232      165     170     175
233 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
234      180     185     190
235 Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
236      195     200     205
237 Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
238      210     215     220
239 Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
240 225     230     235     240
241 Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
242      245     250     255

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243 Val Met Gly Ser Gly Lys
244           260
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248 <211> LENGTH: 1371
249 <212> TYPE: DNA
250 <213> ORGANISM: Lawsonia intracellularis
252 <220> FEATURE:
253 <221> NAME/KEY: CDS
254 <222> LOCATION: (1)...(1368)
256 <400> SEQUENCE: 5
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258 Met Ser Ala Arg Ile Leu Ile Ile Asp Asp Glu Asp Ser Ile Arg Phe
259 1           5           10           15
261 tca ttg aaa gga att ttt gaa gat gag ggc cat gaa gtt tta gaa aga 96
262 Ser Leu Lys Gly Ile Phe Glu Asp Glu Gly His Glu Val Leu Glu Arg
263           20           25           30
265 gct tca gca gaa gaa gga ctt aag tgt gtt gat gta gag tct cca gat 144
266 Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp
267           35           40           45
269 ctt gtt ttt ctt gat att tgg ctt cct ggg atg gat ggt ctt atg gct 192
270 Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
271           50           55           60
273 tta gac cat att cag gct ctt cat cag gaa tta cct gtt att atg att 240
274 Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
275 65           70           75           80
277 tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt 288
278 Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly
279           85           90           95
281 gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att 336
282 Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile
283           100          105          110
285 aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa 384
286 Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys
287           115          120          125
289 tta cta cgt act gta tta cct gag gag agt gag ttt ata gga cag tct 432
290 Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser
291           130          135          140
293 cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca 480
294 Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr
295 145          150          155          160
297 gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta 528
298 Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu
299           165          170          175
301 gct gca caa gca ttg cac aaa gga agc tca cga tat caa aaa cca ttt 576
302 Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe
303           180          185          190
305 ata gct gtt aat tgt gct gct atc cct gaa gaa ttg att gaa agc gaa 624
306 Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu
307           195          200          205

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VERIFICATION SUMMARY

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